

0590
0814

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 10/09/01
Edited by: MM
Verified by: (ST)

DIR

Serial Number: 01915814

Changed a file from non-ASCII to ASCII

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

Edited a formal error in the Current Application Data section, specifically:

Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____

Added the mandatory heading and subheadings for "Current Application Data".

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

Changed the spelling of a mandatory field (the headings or subheadings), specifically: **ENTERED**

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

Inserted colons after headings/subheadings. Headings edited included:

Deleted extra, invalid, headings used by an applicant, specifically:

Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____

Inserted mandatory headings, specifically: _____

Corrected an obvious error in the response, specifically: _____

Edited identifiers where upper case is used but lower case is required, or vice versa.

Corrected an error in the Number of Sequences field, specifically: _____

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/915,814

DATE: 10/09/2001
TIME: 10:40:24

Input Set : A:\PTO.MH.txt
Output Set: N:\CRF3\10092001\I915814.raw

3 <110> APPLICANT: Madeline M. Butler
 4 Andrew T. Watt
 5 Susan M. Freier
 6 Jacqueline Wyatt
 8 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF HORMONE-SENSITIVE LIPASE EXPRESSION
 10 <130> FILE REFERENCE: ISPH-0587
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/915,814
 C--> 12 <141> CURRENT FILING DATE: 2001-07-26
 12 <160> NUMBER OF SEQ ID NOS: 230
 14 <210> SEQ ID NO: 1
 15 <211> LENGTH: 20
 16 <212> TYPE: DNA
 17 <213> ORGANISM: Artificial Sequence
 19 <220> FEATURE:
 20 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓
 22 <400> SEQUENCE: 1
 23 tccgtcatcg ctccctcaggg 20
 25 <210> SEQ ID NO: 2
 26 <211> LENGTH: 20
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial Sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: Antisense Oligonucleotide ✓
 33 <400> SEQUENCE: 2
 34 atgcattctg cccccaagga 20
 36 <210> SEQ ID NO: 3
 37 <211> LENGTH: 3804
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Homo sapiens
 41 <220> FEATURE:
 42 <221> NAME/KEY: CDS
 43 <222> LOCATION: (278)...(3508)
 45 <400> SEQUENCE:
 46 cttcttgtaa gagagtgcta ggcacatagc cccctcttat tcctaattcct cccaccaaag 60
 47 aaaggaggcac agagttcatt acttagtggg ggccagctgt gatcggccaa ctgccagctg 120
 48 cctaaaaaag gaagaccagt gatgcttagga tggagtgaaa cccaagagaga agtgcacatca 180
 49 tggaaatca atgagagatc tgtgaagaga gagggctggg tgggagccca gaaggataga 240
 50 accttggaa tcaatatctc ccgtgaggaa aataaca atg gag cca ggt tct aag 295
 51 Met Glu Pro Gly Ser Lys
 52 1 5
 54 tca gtg tct agg tca gac tgg caa cct gaa cca cac cag agg cct ata 343
 55 Ser Val Ser Arg Ser Asp Trp Gln Pro Glu Pro His Gln Arg Pro Ile
 56 10 15 20
 58 acc ccg cta gag cct ggg cca gaa aag aca ccc ata gcc cag cca gaa 391
 59 Thr Pro Leu Glu Pro Gly Pro Glu Lys Thr Pro Ile Ala Gln Pro Glu
 60 25 30 35
 62 tcg aag act ctg cag gga tcc aat acc caa cag aag cct gct tca aac 439

ENTERED

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63	Ser	Lys	Thr	Leu	Gln	Gly	Ser	Asn	Thr	Gln	Gln	Lys	Pro	Ala	Ser	Asn	
64	40						45					50					
66	caa	aga	ccc	ctc	acc	cag	cag	gag	acc	cct	gca	caa	cat	gat	gct	gaa	487
67	Gln	Arg	Pro	Leu	Thr	Gln	Gln	Glu	Thr	Pro	Ala	Gln	His	Asp	Ala	Glu	
68	55						60					65				70	
70	tcc	cag	aag	gaa	cct	aga	gcc	caa	caa	aaa	tct	gct	tca	caa	gag	gaa	535
71	Ser	Gln	Lys	Glu	Pro	Arg	Ala	Gln	Gln	Lys	Ser	Ala	Ser	Gln	Glu	Glu	
72							75					80				85	
74	ttt	ctt	gcc	cca	cag	aag	ccc	gca	cca	cag	caa	tca	cct	tac	atc	caa	583
75	Phe	Leu	Ala	Pro	Gln	Lys	Pro	Ala	Pro	Gln	Gln	Ser	Pro	Tyr	Ile	Gln	
76							90					95				100	
78	agg	gtg	ctg	ctc	act	caa	cag	gaa	gct	gcc	tcc	cag	cag	gga	cct	ggg	631
79	Arg	Val	Leu	Leu	Thr	Gln	Gln	Glu	Ala	Ala	Ser	Gln	Gln	Gly	Pro	Gly	
80							105					110				115	
82	cta	gga	aaa	gaa	tct	ata	act	caa	cag	gag	cca	gca	ttg	aga	caa	aga	679
83	Leu	Gly	Lys	Glu	Ser	Ile	Thr	Gln	Gln	Glu	Pro	Ala	Leu	Arg	Gln	Arg	
84							120					125				130	
86	cat	gta	gcc	cag	cca	ggg	cct	ggg	cca	gga	gag	cca	cct	cca	gct	caa	727
87	His	Val	Ala	Gln	Pro	Gly	Pro	Gly	Pro	Gly	Glu	Pro	Pro	Pro	Ala	Gln	
88	135						140					145				150	
90	caa	gaa	gct	gaa	tca	aca	cct	gcg	gcc	cag	gct	aaa	cct	gga	gcc	aaa	775
91	Gln	Glu	Ala	Glu	Ser	Thr	Pro	Ala	Ala	Gln	Ala	Lys	Pro	Gly	Ala	Lys	
92							155					160				165	
94	agg	gag	cca	tct	gcc	ccg	act	gaa	tct	aca	tcc	caa	gag	aca	cct	gaa	823
95	Arg	Glu	Pro	Ser	Ala	Pro	Thr	Glu	Ser	Thr	Ser	Gln	Glu	Thr	Pro	Glu	
96							170					175				180	
98	cag	tca	gac	aag	caa	aca	acg	cca	gtc	cag	gga	gcc	aaa	tcc	aag	cag	871
99	Gln	Ser	Asp	Lys	Gln	Thr	Thr	Pro	Val	Gln	Gly	Ala	Lys	Ser	Lys	Gln	
100							185					190				195	
102	gga	tct	ttg	aca	gag	ctg	gga	ttt	cta	aca	aaa	ctt	cag	gaa	cta	tcc	919
103	Gly	Ser	Leu	Thr	Glu	Leu	Gly	Phe	Leu	Thr	Lys	Leu	Gln	Glu	Leu	Ser	
104							200					205				210	
106	ata	cag	cga	tca	gcc	cta	gag	tgg	aag	gca	ctt	tct	gag	tgg	gtc	gca	967
107	Ile	Gln	Arg	Ser	Ala	Leu	Glu	Trp	Lys	Ala	Leu	Ser	Glu	Trp	Val	Ala	
108	215						220					225				230	
110	gat	tct	gag	tca	gaa	tca	gat	gtg	gga	tca	tct	tca	gac	aca	gat	tct	1015
111	Asp	Ser	Glu	Ser	Asp	Val	Gly	Ser	Ser	Ser	Asp	Thr	Asp	Ser			
112							235					240				245	
114	cca	gcc	acg	atg	ggt	gga	atg	gtg	gcc	cag	gga	gtg	aag	cta	ggc	tcc	1063
115	Pro	Ala	Thr	Met	Gly	Gly	Met	Val	Ala	Gln	Gly	Val	Lys	Leu	Gly	Phe	
116							250					255				260	
118	aaa	gga	aaa	tct	ggt	tat	aaa	gtg	atg	tca	gga	tac	agt	ggg	acg	tgc	1111
119	Lys	Gly	Lys	Ser	Gly	Tyr	Lys	Val	Met	Ser	Gly	Tyr	Ser	Gly	Thr	Ser	
120							265					270				275	
122	cca	cat	gag	aaa	acc	agt	gct	cgg	aat	cac	aga	cac	tac	cag	gat	aca	1159
123	Pro	His	Glu	Lys	Thr	Ser	Ala	Arg	Asn	His	Arg	His	Tyr	Gln	Asp	Thr	
124							280					285				290	
126	gcc	tca	agg	ctc	atc	cac	aac	atg	gac	ctg	cgc	aca	atg	aca	cag	tgc	1207
127	Ala	Ser	Arg	Leu	Ile	His	Asn	Met	Asp	Leu	Arg	Thr	Met	Gln	Ser		

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128	295	300	305	310															
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131	Leu	Val	Thr	Leu	Ala	Glu	Asp	Asn	Ile	Ala	Phe	Phe	Ser	Ser	Gln	Gly			
132																	325		
134	cct	ggg	gaa	acg	gcc	cag	cg	ctg	tca	ggc	gtt	ttt	gcc	ggt	gta	cg		1303	
135	Pro	Gly	Glu	Thr	Ala	Gln	Arg	Leu	Ser	Gly	Val	Phe	Ala	Gly	Val	Arg			
136																	340		
138	gag	cag	g	ctg	ggg	ctg	gag	ccg	gcc	ctg	ggc	cg	ctg	ctg	ggt	gt		1351	
139	Glu	Gln	Ala	Leu	Gly	Leu	Glu	Pro	Ala	Leu	Gly	Arg	Leu	Leu	Gly	Val			
140																	355		
142	g	cg	cac	ctc	ttt	gac	ctg	gac	cca	gag	aca	ccg	gcc	aa	ggg	ta	cg		1399
143	Ala	His	Leu	Phe	Asp	Leu	Asp	Pro	Glu	Thr	Pro	Ala	Asn	Gly	Tyr	Arg			
144																	370		
146	agc	cta	gt	ca	ac	aa	cc	cg	tc	tg	cg	ca	ct	ct	ca	aa		1447	
147	Ser	Leu	Val	His	Thr	Ala	Arg	Cys	Cys	Leu	Ala	His	Leu	Leu	His	Lys			
148																	390		
150	tcc	cg	tc	ta	t	gt	g	cc	tc	cg	cg	ac	tc	tt	tc	cg	ac		1495
151	Ser	Arg	Tyr	Val	Ala	Ser	Asn	Arg	Arg	Ser	Ile	Phe	Phe	Arg	Thr	Ser			
152																	405		
154	ca	ac	ct	g	cc	g	ag	ct	g	cc	ta	ct	g	ct	ac	ca	ct		1543
155	His	Asn	Leu	Ala	Glu	Leu	Glu	Ala	Tyr	Leu	Ala	Ala	Leu	Thr	Gln	Leu			
156																	420		
158	cg	g	ct	gt	tc	ta	cc	ca	cg	cg	ct	ct	gt	tt	ac	aa	cg		1591
159	Arg	Ala	Leu	Val	Tyr	Tyr	Ala	Gln	Arg	Leu	Leu	Val	Thr	Asn	Arg	Pro			
160																	435		
162	gg	gta	ct	tt	ttt	gag	gg	gac	gag	gg	ct	ac	cc	gg	gac	tt	ct		1639
163	Gly	Val	Leu	Phe	Phe	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Phe	Leu			
164																	450		
166	cg	gag	ta	gt	ac	ct	ca	a	ag	gg	tg	tt	ta	gg	cg	tg	ct		1687
167	Arg	Glu	Tyr	Val	Thr	Leu	His	Lys	Gly	Cys	Phe	Tyr	Gly	Arg	Cys	Leu			
168																	470		
170	gg	tc	ca	tg	ac	ct	gg	cc	tt	ct	cg	ca	cc	at	tc			1735	
171	Gly	Phe	Gln	Phe	Thr	Pro	Ala	Ile	Arg	Pro	Phe	Leu	Gln	Thr	Ile	Ser			
172																	485		
174	att	gg	ct	gt	tc	tt	gg	gag	ca	ta	aa	cg	aa	gag	aa	gg			
175	Ile	Gly	Leu	Val	Ser	Phe	Gly	Glu	His	Tyr	Lys	Arg	Asn	Glu	Thr	Gly			
176																	500		
178	ct	ca	tg	gt	gg	tc	tt	gg	ca	tc	gg	cc	tt	gg	cg	tc		1831	
179	Leu	Ser	Val	Ala	Ala	Ser	Ser	Leu	Phe	Thr	Ser	Gly	Arg	Phe	Ala	Ile			
180																	515		
182	gac	ccc	gag	ct	cg	ttt	gg	gag	ttt	gag	gg	at	cc	aa	ca	tg		1879	
183	Asp	Pro	Glu	Leu	Arg	Gly	Ala	Glu	Phe	Glu	Arg	Ile	Thr	Gln	Asn	Leu			
184																	530		
186	gac	gt	ca	t	tc	ttt	gg	aa	ttt	gg	ca	cc	aa	ca	gg	at	gg		1927
187	Asp	Val	His	Phe	Trp	Lys	Ala	Phe	Trp	Asn	Ile	Thr	Glu	Met	Glu	Val			
188																	550		
190	cta	tc	tc	tc	gg	aa	at	gca	tc	gg	cc	gt	gg	gg	gt	ag	cg		1975
191	Leu	Ser	Ser	Leu	Ala	Asn	Met	Ala	Ser	Ala	Thr	Val	Arg	Val	Ser	Arg			
192																	565		

RAW SEQUENCE LISTING

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194	ctg	ctc	agc	ctg	cca	ccc	gaa	gcc	ttt	gag	atg	cca	ctg	act	gcc	gac	2023
195	Leu	Leu	Ser	Leu	Pro	Pro	Glu	Ala	Phe	Glu	Met	Pro	Leu	Thr	Ala	Asp	
196				570					575						580		
198	ccc	acg	ctc	acg	gtc	acc	atc	tca	ccc	cca	ctg	gcc	cac	aca	ggc	cct	2071
199	Pro	Thr	Leu	Thr	Val	Thr	Ile	Ser	Pro	Pro	Leu	Ala	His	Thr	Gly	Pro	
200				585				590						595			
202	ggg	ccc	gtc	ctc	gtc	agg	ctc	atc	tcc	tat	gac	ctg	cgt	gaa	gga	cag	2119
203	Gly	Pro	Val	Leu	Val	Arg	Leu	Ile	Ser	Tyr	Asp	Leu	Arg	Glu	Gly	Gln	
204				600				605						610			
206	gac	agt	gag	gag	ctc	agc	agc	ctg	ata	aag	tcc	aac	ggc	caa	cgg	agc	2167
207	Asp	Ser	Glu	Glu	Leu	Ser	Ser	Leu	Ile	Lys	Ser	Asn	Gly	Gln	Arg	Ser	
208	615				620					625					630		
210	ctg	gag	ctg	tgg	ccg	cgc	ccc	cag	cag	gca	ccc	cgc	tcg	cgg	tcc	ctg	2215
211	Leu	Glu	Leu	Trp	Pro	Arg	Pro	Gln	Gln	Ala	Pro	Arg	Ser	Arg	Ser	Leu	
212				635				640						645			
214	ata	gtg	cac	tcc	cac	ggc	ggt	ggc	ttt	gtg	gcc	cag	acc	tcc	aga	tcc	2263
215	Ile	Val	His	Phe	His	Gly	Gly	Gly	Phe	Val	Ala	Gln	Thr	Ser	Arg	Ser	
216				650				655						660			
218	cac	gag	ccc	tac	ctc	aag	agc	tgg	gcc	cag	gag	ctg	ggc	gcc	ccc	atc	2311
219	His	Glu	Pro	Tyr	Leu	Lys	Ser	Trp	Ala	Gln	Glu	Leu	Gly	Ala	Pro	Ile	
220				665				670						675			
222	atc	tcc	atc	gac	tac	tcc	ctg	gcc	cct	gag	gcc	ccc	tcc	ccc	cgt	gcg	2359
223	Ile	Ser	Ile	Asp	Tyr	Ser	Leu	Ala	Pro	Glu	Ala	Pro	Phe	Pro	Arg	Ala	
224				680				685						690			
226	ctg	gag	gag	tgc	tcc	gcc	tac	tgc	tgg	gcc	atc	aag	cac	tgc	gcc	2407	
227	Leu	Glu	Glu	Cys	Phe	Phe	Ala	Tyr	Cys	Trp	Ala	Ile	Lys	His	Cys	Ala	
228	695				700				705					710			
230	ctc	ctt	ggc	tca	aca	ggg	gaa	cga	atc	tgc	ctt	gcg	ggg	gac	agt	gca	2455
231	Leu	Leu	Gly	Ser	Thr	Gly	Glu	Arg	Ile	Cys	Leu	Ala	Gly	Asp	Ser	Ala	
232				715				720						725			
234	ggc	ggg	aac	ctc	tgc	tcc	acc	gtg	gct	ctt	cgg	gca	gca	gcc	tac	ggg	2503
235	Gly	Gly	Asn	Leu	Cys	Phe	Thr	Val	Ala	Leu	Arg	Ala	Ala	Ala	Tyr	Gly	
236				730				735						740			
238	gtg	cgg	gtg	cca	gat	ggc	atc	atg	gca	gcc	tac	ccg	gcc	aca	atg	ctg	2551
239	Val	Arg	Val	Pro	Asp	Gly	Ile	Met	Ala	Ala	Tyr	Pro	Ala	Thr	Met	Leu	
240				745				750						755			
242	cag	cct	gcc	gcc	tct	ccc	tcc	cgc	ctg	ctg	agc	ctc	atg	gac	ccc	ttg	2599
243	Gln	Pro	Ala	Ala	Ser	Pro	Ser	Arg	Leu	Leu	Ser	Leu	Met	Asp	Pro	Leu	
244				760				765						770			
246	ctg	ccc	ctc	agt	gtg	ctc	tcc	aag	tgt	gtc	agc	gcc	tat	gct	ggt	gca	2647
247	Leu	Pro	Leu	Ser	Val	Leu	Ser	Lys	Cys	Val	Ser	Ala	Tyr	Ala	Gly	Ala	
248	775				780				785					790			
250	aag	acg	gag	gac	cac	tcc	aac	tca	gac	cag	aaa	gcc	ctc	ggc	atg	atg	2695
251	Lys	Thr	Glu	Asp	His	Ser	Asn	Ser	Asp	Gln	Lys	Ala	Leu	Gly	Met	Met	
252				795				800						805			
254	ggg	ctg	gtg	cgg	cgg	gac	aca	gcc	ctg	ctc	ctc	cga	gac	tcc	cgc	ctg	2743
255	Gly	Leu	Val	Arg	Arg	Asp	Thr	Ala	Leu	Leu	Leu	Arg	Asp	Phe	Arg	Leu	
256				810				815						820			
258	ggt	gcc	tcc	tca	tgg	ctc	aac	tcc	tcc	ctg	gag	tta	agt	ggg	cgc	aag	2791

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259	Gly	Ala	Ser	Ser	Trp	Leu	Asn	Ser	Phe	Leu	Glu	Leu	Ser	Gly	Arg	Lys	
260	825					830											2839
262	tcc	cag	aag	atg	tcg	gag	ccc	ata	gca	gag	ccg	atg	cgc	cgc	agt	gtg	
263	Ser	Gln	Lys	Met	Ser	Glu	Pro	Ile	Ala	Glu	Pro	Met	Arg	Arg	Ser	Val	
264	840					845										850	
266	tct	gaa	gca	gca	ctg	gcc	cag	ccc	cag	ggc	cca	ctg	ggc	acg	gat	tcc	
267	Ser	Glu	Ala	Ala	Leu	Ala	Gln	Pro	Gln	Gly	Pro	Leu	Gly	Thr	Asp	Ser	
268	855					860										870	
270	ctc	aag	aac	ctg	acc	ctg	agg	gac	ttg	agc	ctg	agg	gga	aac	tcc	gag	
271	Leu	Lys	Asn	Leu	Thr	Leu	Arg	Asp	Leu	Ser	Leu	Arg	Gly	Asn	Ser	Glu	
272						875					880					885	
274	acg	tcg	tcg	gac	acc	ccc	gag	atg	tcg	ctg	tca	gct	gag	aca	ctt	agc	
275	Thr	Ser	Ser	Asp	Thr	Pro	Glu	Met	Ser	Leu	Ser	Ala	Glu	Thr	Leu	Ser	
276	890					895										900	
278	ccc	tcc	aca	ccc	tcc	gat	gtc	aac	ttc	tta	tta	cca	cct	gag	gat	gca	
279	Pro	Ser	Thr	Pro	Ser	Asp	Val	Asn	Phe	Leu	Leu	Pro	Pro	Glu	Asp	Ala	
280	905					910										915	
282	ggg	gaa	gag	gct	gag	gcc	aaa	aat	gag	ctg	agc	ccc	atg	gac	aga	ggc	
283	Gly	Glu	Ala	Glu	Ala	Lys	Asn	Glu	Leu	Ser	Pro	Met	Asp	Arg	Gly		
284	920					925										930	
286	ctg	ggc	gtc	cgt	gcc	gcc	ttc	ccc	gag	ggt	ttc	cac	ccc	cga	cgc	tcc	
287	Leu	Gly	Val	Arg	Ala	Ala	Phe	Pro	Glu	Gly	Phe	His	Pro	Arg	Arg	Ser	
288	935					940					945					950	
290	agc	cag	ggt	gcc	aca	cag	atg	ccc	ctc	tac	tcc	tca	ccc	ata	gtc	aag	
291	Ser	Gln	Gly	Ala	Thr	Gln	Met	Pro	Leu	Tyr	Ser	Ser	Pro	Ile	Val	Lys	
292						955					960					965	
294	aac	ccc	ttc	atg	tcg	ccg	ctg	gca	ccc	gac	agc	atg	ctc	aag	agc		
295	Asn	Pro	Phe	Met	Ser	Pro	Leu	Leu	Ala	Pro	Asp	Ser	Met	Leu	Lys	Ser	
296						970					975					980	
298	ctg	cca	cct	gtg	cac	atc	gtg	gcg	tgc	gctg	gac	ccc	atg	ctg	gac		
299	Leu	Pro	Pro	Val	His	Ile	Val	Ala	Cys	Ala	Leu	Asp	Pro	Met	Leu	Asp	
300						985					990					995	
302	gac	tcg	gtc	atg	ctc	gcg	cgg	cga	ctg	cgc	aac	ctg	ggc	cag	ccg	gtg	
303	Asp	Ser	Val	Met	Leu	Ala	Arg	Arg	Leu	Arg	Asn	Leu	Gly	Gln	Pro	Val	
304						1000					1005					1010	
306	acg	ctg	cgc	gtg	gag	gac	ctg	ccg	cac	ggc	ttc	ctg	acc	cta	gcg		
307	Thr	Leu	Arg	Val	Val	Glu	Asp	Leu	Pro	His	Gly	Phe	Leu	Thr	Leu	Ala	
308	1015					1020					1025					1030	
310	gcg	ctg	tgc	cgc	gag	acg	ccg	cag	gcc	gca	gag	ctg	tgc	gtg	gag	ccg	
311	Ala	Leu	Cys	Arg	Glu	Thr	Arg	Gln	Ala	Ala	Glu	Leu	Cys	Val	Glu	Arg	
312						1035					1040					1045	
314	atc	cgc	ctc	gtc	ctc	act	cct	ccc	gcc	gga	gcc	ggg	ccg	agc	ggg	gag	
315	Ile	Arg	Leu	Val	Leu	Thr	Pro	Pro	Ala	Gly	Ala	Gly	Pro	Ser	Gly	Glu	
316						1050					1055					1060	
318	acg	ggg	gct	gcg	ggg	gta	gac	ggg	ggc	tgc	ggg	ggg	cga	cac	taa		
319	Thr	Gly	Ala	Ala	Gly	Val	Asp	Gly	Gly	Cys	Gly	Gly	Arg	His			
320						1065					1070					1075	
322	aaggcctgttg	ttcccatctg	cgccggcctc	cgtcatgaat	gccttcgggg	ccggggcgaa	3568										
323	ggggacgcgg	gctgtgctta	cttaagtctgg	gggtggcaag	ggggcggggc	ggggccgaa	3628										

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/915,814

DATE: 10/09/2001

TIME: 10:40:25

Input Set : A:\PTO.MH.txt

Output Set: N:\CRF3\10092001\I915814.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date